

SEQUENCE LISTING

<110> VIVIER, ERIC  
MORETTA, ALESSANDRO  
OLCESE, LUCIA  
VELY, FREDERIC  
TOMASELLO, ELENA

<120> NEW POLYPEPTIDES ASSOCIATED WITH ACTIVATORY RECEPTORS  
AND THEIR BIOLOGICAL APPLICATIONS

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<140> 09/403,980  
<141> 2000-01-19

<150> PCT/FR98/00883  
<151> 1998-04-30

<150> FR 97/05411  
<151> 1997-04-30

<150> FR 98/00927  
<151> 1998-01-28

<160> 44

<170> PatentIn Ver. 2.1

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tcc gtg agc cct ggt gta ctg tct ggg att gtt ctg ggt gac ttg gtg 218  
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Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val  
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Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala

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Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val  
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Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg  
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ctatgccat cagggcctg atgcccggat ccggtcattc cagatgccta ctcaacaagc 468  
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<213> Mus musculus

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Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly  
35 40 45

Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro  
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Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn  
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<212> DNA

<213> Mus musculus

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<213> Mus musculus

<220>

<221> MOD\_RES

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<223> Any amino acid

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Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp  
35 40 45

Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ser  
50 55 60

Gly Ile Val Leu Gly Asp Leu Val Thr Leu Leu Ile Ala Leu Ala  
65 70 75 80

Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu  
85 90 95

Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu  
100 105 110

Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg  
115 120 125

Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile Ser Gly Leu Met Pro  
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Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Ser Leu Arg Ser  
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<222> (120)  
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Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly  
35 40 45

Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile  
50 55 60

Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly  
65 70 75 80

Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro  
85 90 95

Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn  
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Pro Gly Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu  
35 40 45

Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly  
50 55 60 1

Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu  
65 70 75 80

Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp  
85 90 95

Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile  
100 105 110

Ser Gly Leu Met Pro Gly Ser Gly His Ser Arg Cys  
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<223> Any amino acid

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50 55 60  
  
Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly  
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Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln  
85 90 95  
  
His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg  
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Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly  
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Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile  
35 40 45

Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly  
50 55 60

Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro  
65 70 75 80

Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn  
85 90 95

Thr Gln Arg Arg Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile Ser Gly  
100 105 110

Leu Met Pro Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Phe  
115 120 125

Cys Gly Ile Arg Thr Pro Val Gly Ile Gln Ile His Arg Val Pro Pro  
130 135 140

Xaa Asp Ile Xaa His Cys Thr Ile Ser Val Pro Lys Xaa Lys Thr Asp  
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<213> Artificial Sequence

<220>  
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<212> PRT  
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<223> Description of Artificial Sequence: Consensus

sequence

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<221> MOD\_RES

<222> (108)

<223> Any amino acid

<400> 17

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Val Ser Pro Gly Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu  
35 40 45

Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser  
50 55 60

Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu  
65 70 75 80

Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr  
85 90 95

Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser Met  
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Pro Ile Ser Gly Leu Met Pro Gly Ser Gly His Ser Arg Cys  
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<210> 18

<211> 2838

<212> DNA

<213> Mus musculus

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<210> 19

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

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<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 20

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21

<210> 21

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<223> Description of Artificial Sequence: Primer

<400> 21  
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<210> 22  
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<223> Description of Artificial Sequence: Primer

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<210> 23  
<211> 21  
<212> DNA  
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<223> Description of Artificial Sequence: Primer

<400> 23  
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<212> DNA  
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<210> 25  
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<212> DNA  
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<212> DNA  
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<223> Description of Artificial Sequence: Primer

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21

<210> 27  
<211> 452  
<212> DNA  
<213> Mus musculus

<220>  
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1 5 10 15

ctg act gtg gag gga tta agt ccc gta cag gcc cag agt gac act ttc 96  
Leu Thr Val Glu Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe  
20 25 30

cca aga tgc gac tgt tct tcc gtg agc cct ggt gta ctg gct ggg att 144  
Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile  
35 40 45

gtt ctg ggt gac ttg gtg ttg act ctg ctg att gcc ctg gct gtg tac 192  
Val Leu Gly Asp Leu Val Thr Leu Leu Ile Ala Leu Ala Val Tyr  
50 55 60

tct ctg ggc cgc ctg gtc tcc cga ggt caa gag agg acc cgg aaa caa 240  
Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln  
65 70 75 80

cac att gct gag act gag tcg cct tat cag gag ctt cag ggt cag aga 288  
His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg  
85 90 95

cat gaa gta tac agt gac ctc aac aca cag agg caa tat tac aga 333  
His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg  
100 105 110

tgagcccaact ctatgcccatt cagcggccctg atgccccggat ccgggtcattc cagatgccta 393

ctcaacaaggc cctctctgag atcaggactc ccgttggaat acagatccac agggtaacct 452

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<212> PRT  
<213> Mus musculus

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Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile  
35 40 45

Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr  
50 55 60

Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln  
65 70 75 80

His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg  
85 90 95

His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg  
100 105 110

<210> 29  
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<220>  
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<400> 29  
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<210> 30  
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<220>  
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<400> 30  
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<210> 31  
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<400> 31  
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tcctgtccag gcccaggccc agagcgattg cagttgctct acggtgagcc cgggcgtgt 180  
ggcagggatc gtgatgggag acctgggtct gacagtgtctc attggccctgg ccgtgtactt 240  
cctggggccgg ctgggtccctc gggggcgagg ggctgcggag gcagcgaccc gaaaaacagcg 300  
tatcaactgag accgagtcgc ctatcagga gctccagggc cagaggtcgg atgtctacag 360  
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gataacctgga t 431

<210> 32  
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<400> 32  
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1 5 10 15

<210> 33  
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<400> 33  
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1 5 10 15

<210> 34  
<211> 15  
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<223> Description of Artificial Sequence: Synthetic peptide

<400> 34  
Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu  
1 5 10 15

<210> 35  
<211> 15  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 35  
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1 5 10 15

<210> 36  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 36  
Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr Ser His Leu  
1 5 10 15

<210> 37  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 37  
Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu  
1 5 10 15

<210> 38  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 38  
Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly Thr Tyr Gln Asp Val  
1 5 10 15

<210> 39  
<211> 15  
<212> PRT  
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<220>  
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<400> 39  
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<210> 40  
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<220>  
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<400> 40  
Tyr Thr Gly Leu Asp Thr Arg Asn Gln Glu Thr Tyr Glu Thr Leu  
1 5 10 15

<210> 41  
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<212> PRT  
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<400> 41  
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<210> 42  
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<220>  
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1 5 10 15

<210> 43  
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<212> PRT  
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<400> 43

Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu  
1 5 10 15  
Leu Thr Val Leu Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe  
20 25 30  
Pro Arg Cys Asp Cys Ser Ser Val Pro Gly Val Leu Ala Gly Ile Val  
35 40 45  
Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Tyr Ser Leu  
50 55 60  
Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln His Ile  
65 70 75 80  
Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu  
85 90 95  
Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg  
100 105

<210> 44  
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20 25 30  
Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile  
35 40 45  
Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Ile  
50 55 60  
Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Glu Arg Thr Arg Lys Gln  
65 70 75 80  
His Ile Ala Arg Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg  
85 90 95  
Pro Glu Val Tyr Ser Asp Leu Arg Thr Gln Arg Gln Tyr Tyr Arg  
100 105 110